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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/821,821

DATE: 04/18/2001
 TIME: 07:50:08

Input Set : A:\36938Aseq.txt
 Output Set: N:\CRF3\04182001\I821821.raw

ENTERED

4 <110> APPLICANT: Welcher, Andrew A.
 5 Calzone, Frank J.
 7 <120> TITLE OF INVENTION: CD20/IgE-Receptor Like Molecules and Uses Thereof
 9 <130> FILE REFERENCE: 01017/36938A
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/821,821
 C--> 12 <141> CURRENT FILING DATE: 2001-03-29
 14 <150> PRIOR APPLICATION NUMBER: US 09/723,258
 15 <151> PRIOR FILING DATE: 2000-11-27
 17 <150> PRIOR APPLICATION NUMBER: US 60/193,728
 18 <151> PRIOR FILING DATE: 2000-03-30
 20 <160> NUMBER OF SEQ ID NOS: 25
 22 <170> SOFTWARE: PatentIn Ver. 2.0
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 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
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 31 <222> LOCATION: (98)..(697)
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 37 Met Asp Ser Ser Thr Ala
 38 1 5
 40 cac agt ccg gtg ttt ctg gta ttt cct cca gaa atc act gct tca gaa 163
 41 His Ser Pro Val Phe Leu Val Phe Pro Pro Glu Ile Thr Ala Ser Glu
 42 10 15 20
 44 tat gag tcc aca gaa ctt tca gcc acg acc ttt tca act caa agc ccc 211
 45 Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro
 46 25 30 35
 48 ttg caa aaa tta ttt gct aga aaa atg aaa atc tta ggg act atc cag 259
 49 Leu Gln Lys Leu Phe Ala Arg Lys Met Lys Ile Leu Gly Thr Ile Gln
 50 40 45 50
 52 atc ctg ttt gga att atg acc ttt tct ttt gga gtt atc ttc ctt ttc 307
 53 Ile Leu Phe Gly Ile Met Thr Phe Ser Phe Gly Val Ile Phe Leu Phe
 54 55 60 65 70
 56 act ttg tta aaa cca tat cca agg ttt ccc ttt ata ttt ctt tca gga 355
 57 Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro Phe Ile Phe Leu Ser Gly
 58 75 80 85
 60 tat cca ttc tgg gcc tct gtt ttg ttc att aat tct gga gcc ttc cta 403
 61 Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile Asn Ser Gly Ala Phe Leu
 62 90 95 100
 65 att gca gtg aaa aga aaa acc aca gaa act ctg ata ata ttg agc cga 451
 66 Ile Ala Val Lys Arg Lys Thr Thr Glu Thr Leu Ile Ile Leu Ser Arg
 67 105 110 115
 69 ata atg aat ttt ctt agt gcc ctg gga gca ata gct gga atc att ctc 499
 70 Ile Met Asn Phe Leu Ser Ala Leu Gly Ala Ile Ala Gly Ile Ile Leu

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73 ctc aca ttt ggt ttc atc cta gat caa aac tac att tgt ggt tat tct 547
74 Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn Tyr Ile Cys Gly Tyr Ser
75 135      140      145      150
77 cac caa aat agt cag tgt aag gct gtt act gtc ctg ttc ttg gga att 595
78 His Gln Asn Ser Gln Cys Lys Ala Val Thr Val Leu Phe Leu Gly Ile
79      155      160      165
81 ttg att aca ttg atg act ttc agc att att gaa tta ttc att tct ctg 643
82 Leu Ile Thr Leu Met Thr Phe Ser Ile Ile Glu Leu Phe Ile Ser Leu
83      170      175      180
85 cct ttc tca att ttg ggg tgc cac tca gag gat tgt gat tgt gaa caa 691
86 Pro Phe Ser Ile Leu Gly Cys His Ser Glu Asp Cys Asp Cys Glu Gln
87      185      190      195
89 tgt tgt tgactagcac tgtgagaata aagatgtgtt aaaatctcaa aaaaaaaaaa 747
90 Cys Cys
91      200
93 aaaaaaaaaa aaa 760
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98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
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103 1      5      10      15
105 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
106      20      25      30
108 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
109      35      40      45
111 Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
112      50      55      60
114 Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
115      65      70      75      80
117 Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
118      85      90      95
120 Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
121      100      105      110
123 Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
124      115      120      125
126 Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
127      130      135      140
129 Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
130 145      150      155      160
132 Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
133      165      170      175
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136      180      185      190
138 Asp Cys Asp Cys Glu Gln Cys Cys
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155                                     Met Leu Leu
156                                     1
158 caa tcc caa acc atg ggg gtt tct cac agc ttt aca cca aag ggc atc 163
159 Gln Ser Gln Thr Met Gly Val Ser His Ser Phe Thr Pro Lys Gly Ile
160      5              10              15
162 act atc cct caa aga gag aaa cct gga cac atg tac caa aac gaa gat 211
163 Thr Ile Pro Gln Arg Glu Lys Pro Gly His Met Tyr Gln Asn Glu Asp
164 20      25              30              35
166 tac ctg cag aac ggg ctg cca aca gaa acc acc gtt ctt ggg act gtc 259
167 Tyr Leu Gln Asn Gly Leu Pro Thr Glu Thr Thr Val Leu Gly Thr Val
168      40              45              50
170 cag atc ctg tgt tgc ctg ttg att tca agt ctg ggg gcc atc ttg gtt 307
171 Gln Ile Leu Cys Cys Leu Leu Ile Ser Ser Leu Gly Ala Ile Leu Val
172      55              60              65
174 ttt gct ccc tac ccc tcc cac ttc aat cca gca att tcc acc act ttg 355
175 Phe Ala Pro Tyr Pro Ser His Phe Asn Pro Ala Ile Ser Thr Thr Leu
176      70              75              80
178 atg tct ggg tac cca ttt tta gga gct ctg tgt ttt ggc att act gga 403
179 Met Ser Gly Tyr Pro Phe Leu Gly Ala Leu Cys Phe Gly Ile Thr Gly
180      85              90              95
182 tcc ctc tca att atc tct gga aaa caa tca act aag ccc ttt gac ctg 451
183 Ser Leu Ser Ile Ile Ser Gly Lys Gln Ser Thr Lys Pro Phe Asp Leu
184 100      105              110              115
186 agc agc ttg acc tca aat gca gtg agt tct gtt act gca gga gca ggc 499
187 Ser Ser Leu Thr Ser Asn Ala Val Ser Ser Val Thr Ala Gly Ala Gly
188      120              125              130
192 ctc ttc ctc ctt gct gac agc atg gta gcc ctg agg act gcc tct caa 547
193 Leu Phe Leu Leu Ala Asp Ser Met Val Ala Leu Arg Thr Ala Ser Gln
194      135              140              145
196 cat tgt ggc tca gaa atg gat tat cta tcc tca ttg cct tat tcg gag 595
197 His Cys Gly Ser Glu Met Asp Tyr Leu Ser Ser Leu Pro Tyr Ser Glu
198      150              155              160
200 tac tat tat cca ata tat gaa atc aaa gat tgt ctc ctg acc agt gtc 643
201 Tyr Tyr Tyr Pro Ile Tyr Glu Ile Lys Asp Cys Leu Leu Thr Ser Val
202      165              170              175
204 agt tta aca ggt gtc cta gtg gtg atg ctc atc ttc act gtg ctg gag 691
205 Ser Leu Thr Gly Val Leu Val Val Met Leu Ile Phe Thr Val Leu Glu
206 180      185              190              195
208 ctc tta tta gct gca tac agt tct gtc ttt tgg tgg aaa cag ctc tac 739
209 Leu Leu Leu Ala Ala Tyr Ser Ser Val Phe Trp Trp Lys Gln Leu Tyr

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210          200          205          210
212 tcc aac aac cct ggg agt tca ttt tcc tcg acc cag tca caa gat cat 787
213 Ser Asn Asn Pro Gly Ser Ser Phe Ser Ser Thr Gln Ser Gln Asp His
214          215          220          225
216 atc caa cag gtc aaa aag agt tct tca cgg tct tgg ata taagtaactc 836
217 Ile Gln Gln Val Lys Lys Ser Ser Arg Ser Trp Ile
218          230          235          240
220 ttggcctcag aggaaggaaa agcaactcaa cactcatggt caagtgtgat tagactttcc 896
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224 atttgaaaaa aaaaaaaaaa aaaaaa 982
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229 <212> TYPE: PRT
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236 Lys Gly Ile Thr Ile Pro Gln Arg Glu Lys Pro Gly His Met Tyr Gln
237 20 25 30
239 Asn Glu Asp Tyr Leu Gln Asn Gly Leu Pro Thr Glu Thr Thr Val Leu
240 35 40 45
242 Gly Thr Val Gln Ile Leu Cys Cys Leu Leu Ile Ser Ser Leu Gly Ala
243 50 55 60
245 Ile Leu Val Phe Ala Pro Tyr Pro Ser His Phe Asn Pro Ala Ile Ser
246 65 70 75 80
248 Thr Thr Leu Met Ser Gly Tyr Pro Phe Leu Gly Ala Leu Cys Phe Gly
249 85 90 95
251 Ile Thr Gly Ser Leu Ser Ile Ile Ser Gly Lys Gln Ser Thr Lys Pro
252 100 105 110
255 Phe Asp Leu Ser Ser Leu Thr Ser Asn Ala Val Ser Ser Val Thr Ala
256 115 120 125
258 Gly Ala Gly Leu Phe Leu Leu Ala Asp Ser Met Val Ala Leu Arg Thr
259 130 135 140
261 Ala Ser Gln His Cys Gly Ser Glu Met Asp Tyr Leu Ser Ser Leu Pro
262 145 150 155 160
264 Tyr Ser Glu Tyr Tyr Tyr Pro Ile Tyr Glu Ile Lys Asp Cys Leu Leu
265 165 170 175
267 Thr Ser Val Ser Leu Thr Gly Val Leu Val Val Met Leu Ile Phe Thr
268 180 185 190
270 Val Leu Glu Leu Leu Leu Ala Ala Tyr Ser Ser Val Phe Trp Trp Lys
271 195 200 205
273 Gln Leu Tyr Ser Asn Asn Pro Gly Ser Ser Phe Ser Ser Thr Gln Ser
274 210 215 220
276 Gln Asp His Ile Gln Gln Val Lys Lys Ser Ser Ser Arg Ser Trp Ile
277 225 230 235 240
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281 <211> LENGTH: 24
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence

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298 <223> OTHER INFORMATION: Description of Artificial Sequence: AP1 Primer
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307 <213> ORGANISM: Artificial Sequence
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318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
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324 <400> SEQUENCE: 8
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328 <210> SEQ ID NO: 9
329 <211> LENGTH: 23
330 <212> TYPE: DNA
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333 <220> FEATURE:
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341 <211> LENGTH: 23
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353 <211> LENGTH: 43
354 <212> TYPE: DNA
355 <213> ORGANISM: Artificial Sequence
357 <220> FEATURE:

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/821,821

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TIME: 07:50:09

Input Set : A:\36938Aseq.txt

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date